REVIEWER INDEX

to Volume 140, May–August, 1995

Below is a list of the people who reviewed manuscripts for GENETICS during the preparation of Volume 140. The aim of GENETICS is to communicate significant research. To succeed, we must recognize what is significant, making sure the presentation is accurate, unambiguous and easily readable. For this, we depend heavily upon our reviewers, who perform this indispensable service without reward. The quality of the journal strongly reflects the quality of their efforts. We apologize to any reviewer whose name has been inadvertently omitted, and we are sincerely grateful to all.

Adams, A.
Adler, P.
Akashi, H.
Albertsen, M.
Alleman, M.
Anderson, K. V.
Appling, D.
Aquadro, C.
Armbruster, P.
Arndt, K.
Arking, R.
Aronow, B. J.
Asmussen, M.

Baker, N.
Ballinger, D.
Barry, E.
Barton, N. H.
Beckenbach, A.
Bellen, H.
Bender, A.
Bennetzen, J.
Berry, A.
Bishop, D.
Botas, J.
Boussy, I.
Breedon, L.
Brilliant, M. H.
Brock, H. W.
Brubaker, C. L.
Brunk, C.
Bryant, P. J.
Bucheton, A.
Buckler, E.
Bürger, R.
Burr, B.
Butow, R.
Byers, B.

Carlson, G.
Carlson, W.
Carr, A.
Casjens, S.
Casselton, L.
Cavener, D. R.
Chang, B.
Charlesworth, B.
Chesser, R.
Chomet, P.
Cooper, T.
Corces, V.
Culbertson, M.

Davis, L.
Dellaporta, S.
DiNardo, S.
Dodds, K.
Doebley, J.
Doerder, F. P.
Drinkwater, N.
Drysdale, C.

Eggleston, W.
Eisen, E. J.
Eissenberg, J.
Elgin, S. C. R.
Elledge, S.
Endow, S.
Enoch, T.
Epperson, B. K.
Estelle, M.
Eyre-Walker, A.

Farabaugh, P.
Feldman, M.
Ferrell, R. E.
Fincham, J.
Flaherty, L.
Fox, G.
Fox, T.
Frankel, W. N.
Franklin, N.
Freeling, M.
Fristrom, J.
Fry, J. D.
Fu, Y-X.

Garrett, S.
Gavazzi, G.
Geyer, P. K.
Gill, B.
Gillespie, J.
Golin, J.
Greene, A.
Gresshoff, P.
Grigliatti, T.
Guthrie, C.
Guttman, D.

Haarar, B.
Haber, J.
Hale, L.
Hall, B. G.
Hampsey, M.
Hamrick, J.
Hannah, C.
Hardy, C.
Harshman, L. G.
Hartl, D.
Hauswirth, W.
Hazelrigg, T.
Helentjaris, T.
Henikoff, S.
Hey, J.
Heywood, J. S.
Hoeschele, I.
Hoffmann, M.
Horai, S.
Houle, D.
Hudson, R.
Huttley, G.

Istock, C.

Jackle, H.
Jahn, C.
Jansen, R. C.
Jiang, C.
Jones, R.
Jorde, L.
Jorgensen, E.

Kaback, D.
Kaiser, C.
Kao, C-H.
Kaplan, N.
Karpen, G.
Karr, T.
Kassis, J. A.
Kaufman, T. C.
Kellogg, E.
Kennison, J. A.
Kidwell, M. G.
Kleckner, N.
Klein, H.
Klobutcher, L.
Knapp, S. J.
Knott, S. A.
Kocher, T. D.
Koltin, Y.
Kondrashov, A. S.
Kozak, C.
Krause, M.
Kreitman, M.
Krider, H.

Lahue, R.
Laipis, P. J.
Lange, K.
Langley, C. H.
Lasko, P.
Last, R. L.
Lawrence, C.
Lee, M.
Lei, C.
Leung, H.
Lewis, P. O.
Liber, H.
Lichten, M.
Liebman, S.
Lindsley, D.
Lis, J.
Livingston, D.
Lloyd, R. G.
Locke, J.
Long, A. D.
Loomis, W.
Loros, J.
Louis, E.
Lyon, M.

MacMorris, P.
Malone, R.
Mangin, B.
Manser, T.
Martienssen, R.
Martindale, D.
Mason, J.
Matson, S.
May, G. S.

McCormick, S.
McGinis, W.
McIntyre, C. L.
McMullen, M.
Meisler, M.
Meneely, P.
Michaelis, S.
Michels, C.
Milkman, R.
Miller, D.
Mitchell-Olds, T.
Mlodzik, M.
Mohler, J.
Montell, D.
Montelone, E.
Moore, P. A.
Moore, S.
Moran, C.
Morton, B. R.
Mosig, G.
Mount, S. M.
Moye-Rowley, W.
Muse, S.
Myers, A.

Neigel, J.
Newlon, C.
Ng, S.
Nikoloff, J.
Nuzhdin, S. V.

Oakley, B. R.
Ochman, H.
O'Connor, M.
Oden, N.
Ohya, Y.
O'Neill, S.
Orr, W.

Paterson, A.
Patterson, G.
Pearlman, R. E.
Petes, T.
Pichersky, E.
Pillen, K.
Platt, T.
Plus, N.
Powell, J.
Prakash, S.
Prout, T.

Quiros, C.

Rabinow, L.
Richards, E.
Richardson, J. P.
Ripley, L. S.
Roberts, J.
Rodin, J.
Rogers, A.
Rosenberg, S.
Russell, P.

Sakonju, S.
Schaaper, R.
Schild, D.
Schnable, P.
Schoen, D.
Schork, N. J.
Scott, W.
Shoemaker, R.
Siede, W.
Silver, L.
Sinden, R. R.
Singh, R.
Siracusa, L.
Skopek, T.
Smith, M.
Sommer, S.
Spofford, J.
Staben, C.
Stam, P.
Stearns, S. C.
Stephan, W.
Stern, M. J.
Strausbaugh, L.
Stuber, C.
Sugawara, N.
Sullivan, W.
Symington, L.
Syvanen, M.
Szauter, P.

Tajima, F.
Tartof, K.
Thompson, E. A.
Tuite, M.
Turelli, M.
Tzagoloff, A.

Uyenoyama, M. K.

Vilgalys, R.
Visscher, P. M.
Volkert, M.

Wakeley, J.
Wallrath, L. L.
Walsh, J. B.
Weil, C.
Weisberg, R.
Werren, J. H.
West, R.
Whitlock, M.
Whittam, T. S.
Wilkinson, G. S.
Wittenberg, C.
Wolfe, K. H.
Wolfner, M.
Woolford, J.
Woolliams, J. A.
Wu, C-I.
Wu, C-T.
Wu, T.

Yedvobnick, B.

Zhivotovsky, L.
Zolan, M.
Zwaan, B.

AUTHOR INDEX

to Volume 140, May–August 1995

Adams, A. E. M., 91
Aigle, M., 945
Aitken, K. S., 418
Alfonso, A., 527
Allis, C. D., 989
Alves, G., 587
Anthony, R. A., 1247
Apolinario, E., 457
Appels, R., 325
Aquadro, C. F., 1019
Arias, T. D., 275
Arnaise, S., 493
Asakawa, S., 1047
Ayala, F. J., 697, 1297
Azevedo, R. B. R., 659

Banks, G. K., 697
Barbujani, G., 811
Barcus, V. A., 1187
Barczak, A. J., 303
Barton, N. H., 821
Beattie, A. E., 703
Beattie, C. W., 703
Begun, D. J., 1019
Beh, K. J., 703
Bender, W., 231
Benito, M.-I., 1087
Bennetzen, J. L., 315
Berloco, M., 615, 1033
Bermingham, E., 275
Bertorelle, G., 811
Bichara, M., 897
Blacketer, M. J., 1259
Blake, K. J., 549
Blows, M. W., 1149
Bohne, B. A., 245
Borts, R. H., 420
Bouchon, B. L., 587
Braverman, J. M., 783
Brickey, W. J., 599
Broom, J. E., 703
Brower, S. M., 91
Brown, P. O., 843
Brown, W. E., 315
Bućan, M., 245
Buitkamp, J., 703
Bulmer, M., 1407
Busson, D., 587

Cano, D. A., 427
Casadesús, J., 427
Cattanach, B. M., 255
Centurion, A., 549
Chandler, V. L., 1087, 1389
Charlesworth, B., 415
Charlesworth, D., 415
Chase, J. W., 435
Cheng, S.-W. C., 875
Chou, T.-B., 231
Cobb, L., 255
Coffino, P., 517
Cohan, F. M., 917
Colby, C., 1129
Comfort, N. C., 1161
Cooke, R., 275
Copeland, N. G., 255, 267
Coppin, E., 493
Corden, J. L., 1223
Cornuet, J.-M., 679
Court, D. L., 875
Crawford, A. M., 703
Cresse, A. D., 315
Crow, J. F., 421
Culley, B. M., 457
Cusset, G., 1289

Dahmann, C., 957
Davies, K., 703
Davis, M. C., 989
Dawes, I. W., 1213
Debuchy, R., 493
Dickinson, M. E., 1061
Dimitri, P., 1033
Dodds, K. G., 703
Dohrmann, P. R., 47
Dubcovsky, J., 1367
Dunn, R. C., 667
Dupuis, J., 843
Dvořák, J., 1367

Ede, A. J., 703
Eichenbaum, Z., 861
Ekechukwu, M. C., 1167
Elena, S. F., 1443
Epperson, B. K., 365, 1431
Epplen, J. T., 703
Estoup, A., 679
Ewens, W. J., 245
Eyre-Walker, A., 1407

Fane, B. A., 1167
Fanti, L., 615
Farman, M. L., 479
Feinstein, P. G., 573
Felsenstein, J., 1421
Feng, W.-Y., 1175
Francis, D. M., 418
Friedman, D. I., 875
Fuchs, R. P. P., 897
Fujita, M., 457
Fujitani, Y., 797
Futcher, B., 957

Garmonsway, H. G., 703
Garnery, L., 679
Garzón, A., 427
Gellon, G., 1339
Gietz, R. D., 443
Giordano, R., 1307
González-Candelas, F., 1443
Gordon, A. J. E., 411
Gorman, M. J., 557
Greenleaf, A. L., 599
Guionneau-Sinclair, F., 275

Halliday, J. A., 411
Halvorson, S., 285
Hardeman, K. J., 1087
Harding, K. W., 1339
Harlow, G. R., 725
Hartl, D. L., 183
Hatzoglou, E., 1353
Hays, J. B., 1175
Hedrick, P., 755
Helfand, S. L., 549
Henikoff, S., 193, 1007
Herrick, G., 989
Hershberger, R. J., 1087
Himeno, H., 1047
Hinata, K., 1099
Hiramine Y., 1235
Hoffman, C. S., 457
Hoffmann, A. A., 1319
Hogan, B. L. M., 1061
Hogness, D. S., 573
Holtsford, T. P., 733
Honts, J. E., 91
Howe, M., 139, 1033
Howell, B., 285
Howell, N., 285
Hudson, R. R., 783
Hulbert, S. H., 315
Hulme, D. J., 703
Hustad, C. M., 255, 267
Hutter, C. M., 537

Iino, Y., 1235
Ikeda, H., 889

Inbar, O., 67
Isogai, A., 1099

Jackson, J. M., 1007
James, A. C., 659
Jenkins, M. E., 725
Jenkins, N. A., 255, 267
Jeune, B., 1289
Jiang, C., 1111
Jiang, Y. W., 47, 103
Jin, M., 457
Johnson, A. D., 79
Johnson, C. D., 527
Johnson, E., 207

Kanik-Ennulat, C., 933
Kaplan, N. L., 783
Kapoun, A. M., 643
Kappes, S. W., 703
Kaufman, T. C., 557, 643
Kaytor, M. D., 1441
Kellogg, E. A., 325
Kirzhner, V. M., 1137
Klämbt, C., 629
Kobayashi, I., 797
Kohli, J., 469
Kolman, C. J., 275
Kornfeld, K., 573
Korol, A. B., 1137
Kovatch, R., 255
Kriticou, D., 697
Kubacka, I., 285
Kubo, K. M., 1389
Kudryashova, E. A., 13
Kuhner, M. K., 1421
Kunz, B. A., 443
Kupiec, M., 1199
Kwiatowski, J., 697

Lamb, B. C., 1277
Lamour-Isnard, C., 587
Langley, C. H., 783
Last, R. L., 303
Laurie, C. C., 667
Lecanidou, R., 1353
Lehmann, E., 469
Leong, S. A., 479
Lewontin, R. C., 377
Li, J., 745
Lichten, M., 55
Lidholm, D.-A., 183
Liebman, S. W., 1247
Liefshitz, B., 1199
Liu, Z., 725
Livingston, D. M., 1441
Livneh, Z., 861
Lohe, A. R., 183
Lord, E. A., 703
Louis, E. J., 420
Lovett, S. T., 27
Lucas, J. R., 315
Lukaszewski, A. J., 1069

Ma, J., 725
Mackey, D., 285
Macrae, M., 517
Madaule, P., 1259
Maddox, J. F., 703
Madhu, W., 79
Mann, R. S., 573
Martin, K., 67
Martin-Morris, L. E., 193
Matthew, P., 703
Matthews, M. E., 703
Maundrell, K., 457
Maya, R., 1199
McCullough, D. A., 285
McGill, C. B., 965
McGinnis, N., 1339
McGinnis, W., 1339
McGraw, R. A., 703
Mestres, F., 1297
Mikula, B. C., 1379
Mitchell-Olds, T., 1105
Miura, K.-I., 1047
Montalvo, E., 933
Montgomery, G. W., 703
Morton, N. E., 7
Mount, D. W., 725
Moya, A., 1443
Murray, N. E., 1187
Myers, A. M., 1259

Nagoshi, R., 207
Naprta, B., 549
Neff, N., 933
Ness, F., 945
Nguyen, M., 527, 1441
Nguyen, T. C., 703
Nolan, P. M., 245

Oberste, D. J., 1167
Ohtake, Y., 129
O'Neill, S. L., 1307
Orr, H. A., 389

Parket, A., 67, 1199
Partridge, L., 659
Patterson, B., 505
Patterson, G. I., 1389
Penty, J. M., 703
Perez, D. E., 201
Perry, W. L., 255, 267
Pham, A., 587
Philippsen, P., 973
Phillips, C. A., 767
Picard, M., 493
Pickard, G. E., 245
Pierson, C. A., 703
Pimpinelli, S., 615
Plasterk, R. H. A., 517
Plugina, L. A., 13
Podolsky, R. H., 733
Préat, T., 587
Pruitt, K. D., 303
Purugganan, M. D., 345

Rand, D. M., 537
Rand, J. B., 527
Rasberry, C., 255
Raymond, M., 1413
Roberts, M. S., 917
Robertson, H. M., 1307
Robinson, A. S., 697
Roche, H., 443
Rodakis, G. C., 1353
Rogina, B., 549
Ronin, Y. I., 1137
Rooks, R. S., 435
Rounsley, S. D., 345
Rousset, F., 1413
Routman, E., 767

St. Clair, D. A., 418
Satta, Y., 1099
Savolainen, O., 755
Scherbakov, V. P., 13
Schild, D., 115
Schmidt, R. J., 345
Schrick, J. J., 1061
Schubiger, G., 219
Schumacher, S., 897
Schwaiger, W., 703
Scott, M. J., 697
Selby, P. B., 1061
Serra, L., 1297
Shafer, B. K., 965
Shafer, K. S., 435
Shimizu, H., 889
Shotwell, M. A., 725
Shroyer, T., 1389
Siegmund, D., 843
Sinclair, D. A., 1213
Siracusa, L. D., 255
Sokolowski, M. B., 1149
Solignac, M., 679
Sollars, P. J., 245
Soto, M. C., 231
Spinelli, L., 615
Spudich, J. A., 505
Steiner, S., 973

Stephan, W., 783
Stigler, S. M., 857
Stillman, D. J., 47, 103
Stone, R. T., 703
Stracks, M. D., 549
Strathern, J. N., 965
Sutera, V. A., Jr., 27
Swing, D. A., 267

Talbert, P. B., 1007
Tamkun, J. W., 615
Tanksley, S. D., 745
Templeton, A. R., 403, 767
Thaler, D. S., 909
Therond, P., 587
Thomas-Orillard, M., 1289
Thorsness, P. E., 435
Titheradge, A. J. B., 1187
Tombline, G., 909
Tomkiel, J., 615
Tournier, F. B., 587
Tricoire, H., 587
Turelli, M., 389, 1319

Wakimoto, B. T., 219, 615, 1033
Walbot, V., 1087
Wang, J., 357
Ward, J. G., 989
Ward, R. H., 275
Warren, C., 1087
Watanabe, K., 1047
Watanabe, M., 1099
Wayne, S., 207
Weber, E. R., 435
Wemmer, T., 629
Wendland, J., 973
West, M. L., 1223
Wickner, R. B., 129
Williams, S. M., 1129
Woychik, R. P., 1061
Wright, M. C., 973
Wu, C.-I, 201
Wu, C.-T., 139
Wu, T.-C., 55

Xiao, J., 745

Yamaguchi, H., 889
Yamakawa, S., 1099
Yamamoto, K., 797
Yamamoto, M., 457, 1235
Yamato, J., 1421
Yanofsky, M. F., 345
Yasuda, G. K., 219
Yuan, L., 745

Zahn, K., 909
Zahn-Zabal, M., 469
Zawadzki, P., 917
Zeng, Z.-B., 1111
Zhao, J., 303
Zickler, D., 493
Zwolinski, S. A., 1277

SUBJECT INDEX

to Volume 140, May–August 1995

Acetylcholinesterase inhibitors, resistance of *Caenorhabditis elegans* mutants, 527
Achilles' cleavage (AC) technique, telomere mapping in *Magnaporthe grisea*, 479
Actin, fimbrin-actin binding interaction in *Saccharomyces cerevisiae*, 91
Adaptation, nuclear-cytoplasmic coadaptation in *Drosophila*, 537
Age/aging, gene expression during aging in adult *Drosophila melanogaster*, 549
Agouti protein activity assay, 267
Albinaria coerulea, sequence and gene organization of mitochondrial genome, 1353
Alcohol dehydrogenase, *Adh* gene expression in *Drosophila melanogaster*, effects of transposable element insertion, 667
Alleles
  agouti recessive mutations, 255
  allelic diversity at *hsd* locus in *Escherichia coli*, 1187
  ApoEε4 allele and Alzheimer's disease, cladistic analysis, 403
  detection of linkage disequilibrium in sequences, 377
  lethal-gene allelism in *Drosophila subobscura* colonizing America, 1297
  rad52-20 suppression by *RAD1* and *MAT*, 115
Allozymes, population structure in *Clarkia dudleyana*, comparison of population differentiation (F_{ST}) between allozymes and morphological traits, 733
Alzheimer's disease, apolipoprotein E locus in, cladistic analysis, 403
Amblystoma tigrinum, geographic distribution of mtDNA haplotypes, cladistic analysis, 767
Antirrhinum majus, MADS-Box regulatory gene family, molecular evolution, 345
Apis mellifera, subspecies, microsatellite variation in, 679
Apolipoprotein E, Alzheimer's disease and, cladistic analysis of phenotypes, 403
Arabidopsis, interval mapping of heterosis viability loci in, 1105
Arabidopsis thaliana
  MADS-Box regulatory gene family, molecular evolution, 345
  radiation-sensitive mutants, 725
  tryptophan synthase beta subunit mutants, 303
Ascobolus immersus, selection for gene conversion frequencies in, polygenes and, 1277
Ashbya gossypii, DNA integration and rearrangements, homologous recombination and, 973
Asterina pectinifera, nucleotide sequence and gene organization of mitochondrial genome, 1047
Autocorrelation index for DNA analysis (AIDA), spatial patterns of DNA diversity, 811
Bacillus, sexual isolation and sequence divergence in *Bacillus* transformation, 917
Bacteria
  Escherichia coli. *See Escherichia coli*
  sexual isolation and sequence divergence in *Bacillus* transformation, 917
  synonymous substitution rates in enterobacteria, 1407
Bacteriophage
  bacteriophage ϕX174 mutations affecting morphogenesis of 50S complex, 1167
  Erf recombinase in bacteriophage P22-mediated plasmid transduction, 427
  λ *bio* transducing phage produced by oxolinic acid-induced illegitimate recombination, 889
  marker-dependent recombination in T4 bacteriophage, T4 DNA polymerase in, 13
  Rho-dependent transcription terminators in *nin* region of bacteriophage λ, 875
Behavior, circling/waltzing behavior, mouse *Wheels* mutation, 245
Brassica, self-incompatibility system, *S*-related genes, 1099

Caenorhabditis elegans
  mutants, resistance to acetylcholinesterase inhibitors, 527
  ornithine decarboxylase gene of, 517
Carboxy-terminal repeat domain (CTD)
  RNA polymerase II
    Drosophila, 599
    mutations in yeast, 1223
  in transcription, 1223
Cellular differentiation, *Saccharomyces cerevisiae*, α2 repression and, 79
Cellular morphogenesis, in *Saccharomyces cerevisiae*, 1259
Ceratitis capitata, second superoxide dismutase (*Sod*) gene, 697
Chromatid, breakage-fusion-bridge cycle in wheat, 1069
Chromatin, organization, yeast *SIN4-RGR1* complex in, 47
Chromosome
  breakage-fusion-bridge cycle in wheat, 1069
  lethal-gene allelism and chromosome arrangements in *Drosophila subobscura* colonizing America, 1297
  mouse *Wheels* mutation locus mapped to chromosome 4, 245
  nullisomic chromosome deficiencies, effect on conjugation in *Tetrahymena thermophila*, 989
  pairing, sensitivity of regulatory regions of *proboscipedia* homeotic gene, 643
Cladistic analysis
  case/control data, Alzheimer's disease and apolipoprotein E locus, 403

geographic distribution of mtDNA haplotypes in *Amblystoma tigrinum*, 767
Clarkia dudleyana, population structure, comparison of population differentiation (F_{ST}) between allozymes and morphological traits, 733
Cloning
abnormal oocyte (abo) gene of *Drosophila melanogaster*, 615
ornithine decarboxylase gene of *Caenorhabditis elegans*, 517
Cold Spring Harbor Symposium (1951) (*Perspectives*), 1161
Committee on Biological Effects of Atomic Radiation (BEAR), quarreling geneticists and a diplomat (*Perspectives*), 421
Conjugation, in *Tetrahymena thermophila*, effect of nullisomic chromosome deficiencies, 989
Conversion, polygenes and selection for gene conversion frequencies in *Ascobolus immersus*, 1277
Cyclins, B-type, specialization for mitosis or meiosis in *Saccharomyces cerevisiae*, 957
Cytoplasmic incompatibility
in *Drosophila sechellia* and *D. mauritiana*, 1307
in *Drosophila simulans*, 1319

Detergent resistance, vanadate-resistant mutants of *Saccharomyces cerevisiae*, 933
Dictyostelium, positive selection for cold-sensitive myosin heavy chain mutants, 505
DNA
approximate variance of nucleotide divergence between two sequences estimated from restriction fragment data (*letter*), 1443
double-strand breaks
DNA synthesis errors in recombinational repair in *Saccharomyces cerevisiae*, 965
meiosis-induced, in *Saccharomyces cerevisiae*, 55
recombination of Ty elements in *Saccharomyces cerevisiae*, 67
hitchhiking effect on site frequency spectrum of DNA polymorphisms in *Drosophila*, 783
integration and rearrangements in *Ashbya gossypii*, homologous recombination and, 973
inversions with deletions and duplications, 411
mitochondrial
fitness of mtDNA in *Drosophila pseudoobscura vs. D. psersimilis*, 537
geographic distribution of mtDNA haplotypes in *Amblystoma tigrinum*, cladistic analysis, 767
mtDNA haplotype diversity, in Ngöbé Amerinds of Panama, 275
nucleotide sequence of *Albinaria coerulea*, 1353
nucleotide sequence of *Asterina pectinifera*, 1047
phylogenetic analysis of mitochondrial genomes from Leber hereditary optic neuropathy, 285
suppression of *yme1* rho^0 slow growth in *Saccharomyces cerevisiae*, 435
Mu1 insertional specificity in low copy number DNA, 315
spatial patterns of DNA diversity, autocorrelation indices for DNA analysis, 811
DNA gyrase, -mediated oxolinic acid-induced illegitimate recombination in *Escherichia coli*, 889
DNA markers
microsatellite variation in *Apis mellifera* populations, 679
mitochondrial DNA. *See* DNA, mitochondrial
random amplified polymorphic DNA (RAPD). *See* Random amplified polymorphic DNA (RAPD)
DNA polymerase, T4, in recombination, 13
DNA repair
double-strand breaks, DNA synthesis errors in recombinational repair in *Saccharomyces cerevisiae*, 965
recombinagenic mismatch repair of UV-irradiated DNA, 1175
role of *RAD* genes in recombination between repeated sequences in yeast, 1199
DNA synthesis
bacteriophage ϕX174 mutations affecting morphogenesis of 50S complex, 1167
errors, in double-strand break repair in *Saccharomyces cerevisiae*, 965
Dominance complementation, genetic basis of heterosis in rice, 745
Dominance theory, Haldane's rule, 389
Drosophila
analysis of *bulge, argos* and *soba* genes, 629
behavior of *brown*$^{\text{Dominant}}$ (bw$^{\text{D}}$) heterochromatic element, distance and pairing effects, 1007
cytoplasmic incompatibility in *Drosophila sechellia* and *D. mauritiana*, 1307
cytoplasmic incompatibility in *Drosophila simulans*, 1319
fitness of mtDNA in *Drosophila pseudoobscura vs. D. psersimilis*, 537
lethal-gene allelism in *Drosophila subobscura* colonizing America, 1297
modifiers of *Deformed (Def)* function in, 1339
nucleotide variation at *vermilion* locus in geographically diverse *Drosophila melanogaster* and *D. simulans* populations, 1019
Odysseus locus of hybrid-male sterility in *Drosophila*, 201
RNA polymerase II, carboxy-terminal repeat domain (CTD) function, 599
Drosophila C virus, susceptibility/resistance of *Drosophila melanogaster*, 1289
Drosophila melanogaster
abnormal oocyte (abo) gene, 615
alcohol dehydrogenase gene expression, effects of transposable element insertion, 667
expression of additive genetic variation under stress, 1149

gene expression during aging in adult *Drosophila melanogaster*, 549
germline mosaics of Polycomb group, 231
heterochromatic and euchromatic gene activity in, *cis*-effects of heterochromatin, 1033
hitchhiking effect on site frequency spectrum of DNA polymorphisms in, 783
homeotic target genes, 573
latitudinal cline in body size, 659
ms(3)K81, paternal effect gene, 219
ovary follicle cell differentiation, *fs(1)Yb* and *Notch* gene interactions, 207
regulatory elements of homeotic gene *Sex combs reduced (Scr)*, 557
regulatory regions of *proboscipedia* homeotic gene, 643
Suppressor of fused [su(fu)] gene, 587
Suppressor 2 of zeste complex [su(z)2-C], 139
susceptibility/resistance to Drosophila C virus, 1289
trans-inactivation of *brown* gene, 193

Effective population size
estimation, Metropolis-Hastings sampling, 1421
partially sib-mated population, 357
Embryogenesis, *ms(3)K81*, paternal effect gene of *Drosophila melanogaster*, 219
Environment
expression of additive genetic variation under stress in *Drosophila melanogaster*, 1149
latitudinal cline in body size of *Drosophila melanogaster*, 659
programmed heritable change in *r*-gene expression using temperature and light at specific developmental stages in maize seedlings, 1379
Escherichia coli
allelic diversity at *hsd* locus in *Escherichia coli*, 1187
CpG monotonous runs, genetic instability, 897
DNA gyrase-mediated oxolinic acid-induced illegitimate recombination in, 889
recJ suppression by alterations in DNA helicases, 27
short-patch reverse transcription, 909
Evolution
linkage and limits to natural selection, 821
S-related genes of *Brassica* self-incompatibiity system, 1099
Exonucleases, in recombinagenic mismatch repair of UV-irradiated DNA, 1175

Fimbrin, fimbrin-actin binding interaction in *Saccharomyces cerevisiae*, 91
Fingerprints, Galton and identification by fingerprints (*Perspectives*), 957
Fisher's exact test, detection of linkage disequilibrium in sequences, 377
Fitness
fitness of mtDNA in *Drosophila pseudoobscura vs. D. psersimilis*, 537
quantitative traits, association with heterozygosity, in Scots pine, 755
Flowering plants, molecular evolution of plant MADS-Box regulatory gene family, 345
5-Fluoroindole, resistance, tryptophan synthase beta subunit mutants in *Arabidopsis thaliana*, 303

Galton, Francis, identification by fingerprints (*Perspectives*), 957
Gene(s)
abnormal oocyte (abo) gene of *Drosophila melanogaster*, 615
alcohol dehydrogenase gene expression in *Drosophila melanogaster*, effects of transposable element insertion, 667
allelic diversity at *hsd* locus in *Escherichia coli*, 1187
analysis of *bulge*, *argos* and *soba* genes of *Drosophila*, 629
ARE, α2 repression in *Saccharomyces cerevisiae*, 79
Caenorhabditis elegans neurotransmitter genes, 527
ccSod1 and *ccSod2* genes in *Ceratitis capitata*, 697
cdc2 and other genes in meiosis in *Schizosaccharomyces pombe*, 1235
conservation of *trans*-inactivation of *brown* gene in *Drosophila*, 193
ELM genes and pseudohyphal differentiation in *Saccharomyces cerevisiae*, 1259
fs(1)Yb and *Notch* interactions, ovary follicle cell differentiation, 207
gene expression during aging in adult *Drosophila melanogaster*, 549
germline mosaics of Polycomb group of *Drosophila melanogaster*, 231
heterochromatic and euchromatic gene activity in *Drosophila melanogaster*, 1033
homeotic target genes of *Drosophila melanogaster*, 573
KRB1, second copy of *RPL4B* on fragment of chromosome *XII*, 129
lethal-gene allelism in *Drosophila subobscura* colonizing America, 1297
MADS-Box regulatory gene family of flowering plants, molecular evolution, 345
mat genes in karyogamy, meiosis, and sporulation in *Podospora anserina*, 493
modifiers of *Deformed (Def)* function in *Drosophila*, 1339
ms(3)K81, paternal effect gene of *Drosophila melanogaster*, 219
nucleotide sequence and gene organization of *Albinaria coerulea* mitochondrial genome, 1353
nucleotide sequence and gene organization of *Asterina pectinifera* mitochondrial genome, 1047
nucleotide variation at *vermilion* locus in geographically diverse *Drosophila melanogaster* and *D. simulans* populations, 1019
Odysseus locus of hybrid-male sterility in *Drosophila*, 201

ornithine decarboxylase gene of *Caenorhabditis elegans*, 517
paramutation of maize *b* gene, sequences required for, 1389
polygenes and selection for gene conversion frequencies in *Ascobolus immersus*, 1277
programmed heritable change in *r*-gene expression using temperature and light at specific developmental stages in maize seedlings, 1379
rad52-20 suppression by *RAD1* and *MAT*, 115
recJ suppression by alterations in DNA helicases, 27
regulatory regions of *proboscipedia* homeotic gene, sensitivity to chromosome pairing, 643
REV dependency of *rad* mutators in *Saccharomyces cerevisiae*, 443
ribosomal RNA multigene loci in wheat, 1367
role of *RAD* genes in recombination repair between repeated sequences in yeast, 1199
RTM1 (resistance to toxic molasses), new telomeric yeast gene, 945
sck1 (suppressor of loss of cAMP-dependent protein kinase activity) gene, 457
second superoxide dismutase (*Sod*) gene in *Ceratitis capitata*, 697
Sex combs reduced (Scr), regulatory elements, 557
SIN4 regulation of *HIS4* expression in *Saccharomyces cerevisiae*, 103
SIN4-RGR1 complex in chromatin organization and transcriptional regulation in *Saccharomyces cerevisiae*, 47
S-related genes of *Brassica* self-incompatibiity system, 1099
5S RNA genes, intraspecific and intraspecific variation, 325
Suppressor 2 of zeste complex [su(z)2-C] of *Drosophila melanogaster*, 139
synonymous substitution rates in enterobacteria, 1407
Genome
autosomal genetic linkage map of sheep genome, 703
mitochondrial
nucleotide sequence and gene organization of *Albinaria coerulea*, 1353
nucleotide sequence and gene organization of *Asterina pectinifera*, 1047
phylogenetic analysis of mitochondrial genomes from Leber hereditary optic neuropathy, 285
Genotype
spatial distributions of genotypes under isolation by distance, 1431
spatial structure of two-locus genotypes under isolation by distance, 365
Germline, germline mosaics of Polycomb group of *Drosophila melanogaster*, 231
Glycine catabolism, *Saccharomyces cerevisiae*, 1213
Glycine decarboxylase multienzyme complex, *Saccharomyces cerevisiae*, 1213
Growth and development
latitudinal cline in body size of *Drosophila melanogaster*, 659
molecular evolution of plant MADS-Box regulatory gene family, 345
ornithine decarboxylase gene of *Caenorhabditis elegans*, 517
suppression of *yme1* rho^0 slow growth in *Saccharomyces cerevisiae*, 435

Haldane's rule, dominance theory, 389
Haplotype
geographic distribution of mtDNA haplotypes in *Ambystoma tigrinum*, cladistic analysis, 767
mitochondrial DNA haplotype diversity, in Ngöbé Amerinds of Panama, 275
Hardy-Weinberg proportions, 1413
Helicase(s)
alterations, *recJ* suppression, 27
in recombinagenic mismatch repair of UV-irradiated DNA, 1175
Heterochromatin
cis-effects on heterochromatic and euchromatic gene activity in *Drosophila melanogaster*, 1033
distance effect, behavior of *brown*$^{\text{Dominant}}$ (bw$^{\text{D}}$) heterochromatic element in *Drosophila*, 1007
Heterosis
genetic basis in rice, dominance complementation, 745
interval mapping of heterosis viability loci in *Arabidopsis*, 1105
Heterozygosity
association of fitness traits, in Scots pine, 755
mating-type, suppression of *rad52-20*, 115
Heterozygote deficiency, 1413
Hitchhiking
effect on site frequency spectrum of DNA polymorphisms in *Drosophila*, 783
limits to natural selection, 821
Hybrids
genetic basis of heterosis in rice, dominance complementation, 745
Haldane's rule, 389
Odysseus locus of hybrid-male sterility in *Drosophila*, 201

Identity by descent, multilocus model for linkage analysis of complex traits, 843
Inactivation, conservation of *trans*-inactivation of *brown* gene in *Drosophila*, 193
Inbreeding
relationship between mating system and Lyt element abundance in (*letter*), 418
transposable elements in inbreeding and outbreeding populations (*letter*), 415
Inbreeding coefficient, recurrence equation for inbreeding coefficient for partially sib-mated population, 357

Incompatibility
cytoplasmic incompatibility in *Drosophila sechellia* and *D. mauritiana*, 1307
cytoplasmic incompatibility in *Drosophila simulans*, 1319
Infinite allele model, microsatellite variation in *Apis mellifera* populations, 679
Instability, CpG monotonous runs and frameshift mutations in *Escherichia coli*, 897
Isolation by distance
spatial distributions of genotypes under, 1431
spatial structure of two-locus genotypes under isolation by distance, 365
I statistics, spatial structure of two-locus genotypes under isolation by distance, 365

Join-count statistics, spatial structure of two-locus genotypes under isolation by distance, 365

Karyogamy, in *Podospora anserina*, *mat* genes in, 493
Kimura, Motoo (*In Memoriam*), 1

Lateral inhibition, 629
Leber hereditary optic neuropathy, phylogenetic analysis of mitochondrial genomes, 285
Light exposure
programmed heritable change in *r*-gene expression using temperature and light at specific developmental stages in maize seedlings, 1379
radiation-sensitive mutants of *Arabidopsis thaliana*, 725
Linkage
autosomal genetic linkage map of sheep genome, 703
detection of linkage disequilibrium in sequences, 377
limits to natural selection, 821
LODs past and present (*Perspectives*), 7
Linkage analysis, multilocus model for linkage analysis of complex traits, 843
LOD (logarithm of odds), past and present (*Perspectives*), 7
Lycopersicon spp.
relationship between mating system and Lyt element abundance in (*letter*), 418
transposable elements in inbreeding and outbreeding populations (*letter*), 415

Magnaporthe grisea, telomere mapping, 479
Maize
homologous transcripts encoded by *MuDR* transposable element, 1087
Mu1 insertional specificity, 315
Mutator transposable element system, 315
paramutation of maize *b* gene, sequences required for, 1389
programmed heritable change in *r*-gene expression using temperature and light at specific developmental stages in maize seedlings, 1379
Mapping
autosomal genetic linkage map of sheep genome, 703
deletion mapping of heterochromatin in *Drosophila melanogaster*, 1033
heterozygosity mapping of mouse *Wheels* mutation, 245
interval mapping of heterosis viability loci in *Arabidopsis*, 1105
interval mapping of QTL employing correlated trait complexes, 1137
mapping QTL on multiple traits, 1111
Odysseus locus of hybrid-male sterility in *Drosophila*, 201
ornithine decarboxylase gene of *Caenorhabditis elegans*, 517
sequences required for paramutation of maize *b* gene, 1389
telomeres, in *Magnaporthe grisea*, 479
Mating type, *mat* genes in karyogamy, meiosis, and sporulation in *Podospora anserina*, 493
McClintock, Barbara, Cold Spring Harbor Symposium (1951) (*Perspectives*), 1161
Meiosis
-induced double-strand DNA breaks in *Saccharomyces cerevisiae*, 55
in *Podospora anserina*, *mat* genes in, 493
Saccharomyces cerevisiae, B-type cyclins for, 957
Schizosaccharomyces pombe, *cdc2* and other genes in, 1235
Metropolis-Hastings sampling, effective population size times mutation rate per site, 1421
Mice
agouti protein activity assay, 267
agouti recessive mutations, 255
heterozygosity mapping of mouse *Wheels* mutation, 245
mouse *TgN(Imusd)370Rpw* tail mutation, 1061
Mismatch repair (MMR)
recombinagenic mismatch repair of UV-irradiated DNA, 1175
T4 DNA polymerase in, 13
Mitochondria
mitochondrial DNA. *See also* DNA, mitochondrial
mitochondrial DNA haplotype diversity, in Ngōbé Amerinds of Panama, 275
phylogenetic analysis of mitochondrial genomes from Leber hereditary optic neuropathy, 285
suppression of *yme1* rho^0 slow growth in *Saccharomyces cerevisiae* by mutations in mitochondrial ATP synthase gamma subunit, 435
Mitosis, *Saccharomyces cerevisiae*, B-type cyclins for, 957
Models/modeling
effect of adaptive mutagenesis on genetic variation at a linked, neutral locus, 1129
frequency of homologous recombination, dependence on homology length, 797
hitchhiking effect on site frequency spectrum of DNA polymorphisms in *Drosophila*, 783

mapping QTL on multiple traits, 1111
microsatellite variation in *Apis mellifera* populations, 679
multilocus model for linkage analysis of complex traits, 843
spatial distributions of genotypes under isolation by distance, 1431
spatial structure of two-locus genotypes under isolation by distance, 365
Moran's I statistics. *See* I statistics
Mutagenesis
adaptive, effect on genetic variation at a linked, neutral locus, 1129
DNA synthesis errors in recombinational repair of double-strand breaks in *Saccharomyces cerevisiae*, 965
ornithine decarboxylase gene of *Caenorhabditis elegans*, 517
Mutants
Caenorhabditis elegans, resistance to acetylcholinesterase inhibitors, 527
positive selection for cold-sensitive myosin heavy chain mutants in Dictyostelium, 505
radiation-sensitive mutants of *Arabidopsis thaliana*, 725
tryptophan synthase beta subunit mutants in *Arabidopsis thaliana*, 303
vanadate-resistant mutants of *Saccharomyces cerevisiae*, protein glycosylation, sporulation and detergent resistance, 933
yeast morphologic mutants, 1259
Mutation
abnormal oocyte (abo) gene of *Drosophila melanogaster*, 615
agouti protein activity assay, 267
agouti recessive mutations, 255
bacteriophage ϕX174 mutations affecting morphogenesis of 50S complex, 1167
carboxy-terminal repeat domain (CTD), of RNA polymerase II, 1223
CpG monotonous runs and frameshift mutations in *Escherichia coli*, 897
effective population size times mutation rate per site, Metropolis-Hastings sampling, 1421
heterozygosity mapping of mouse *Wheels* mutation, 245
inversions with deletions and duplications, 411
M26 mutation in *Schizosaccharomyces pombe*, 469
mouse *TgN(Imusd)370Rpw* tail mutation, 1061
Mu1 insertional specificity in low copy number DNA, 315
phylogenetic analysis of mitochondrial genomes from Leber hereditary optic neuropathy, 285
Polycomb group, germline mosaics, 231
REV dependency of *rad* mutators in *Saccharomyces cerevisiae*, 443
suppression of *yme1* rho^0 slow growth in *Saccharomyces cerevisiae*, 435
Suppressor of fused [su(fu)] gene, 587
Suppressor 2 of zeste complex [su(z)2-C] of *Drosophila melanogaster*, 139
Myosin, positive selection for cold-sensitive myosin heavy chain mutants in Dictyostelium, 505

Neurotransmission, in *Caenorhabditis elegans*, 527
Ngŏbé Amerinds, mtDNA haplotype diversity, 275
Nucleolus organizing regions (NORs), wheat, 1367

Oogenesis, *fs(1)Yb* in *Drosophila*, 207
Ornithine decarboxylase, *Caenorhabditis elegans*, 517
Orr's multiplicative model, 389
Orthovanadate, 933
Ovary, follicle cell differentiation, *fs(1)Yb* and *Notch* gene interactions, 207
Oxolinic acid, -induced illegitimate recombination, lambda *bio* transducing phage produced by, 889

Paramutation
maize *b* gene, sequences required for, 1389
programmed heritable change in *r*-gene expression using temperature and light at specific developmental stages in maize seedlings, 1379
Perspectives
Galton and identification by fingerprints, 857
LODs past and present, 7
quarreling geneticists and a diplomat, 421
two genes, no enzyme: second look at Barbara McClintock and 1951 Cold Spring Harbor Symposium, 1161
Phenotype
cladistic analysis of phenotypes, Alzheimer's disease and apolipoprotein E, 403
mouse *TgN(Imusd)370Rpw* tail mutation, 1061
Plasmids, Erf-mediated plasmid transduction, 427
Podospora anserina, *mat* genes in karyogamy, meiosis, and sporulation in, 493
Polygenes, selection for gene conversion frequencies in *Ascobolus immersus*, 1277
Polymorphism
detection of linkage disequilibrium in sequences, 377
hitchhiking effect on site frequency spectrum of DNA polymorphisms in *Drosophila*, 783
restriction fragment length. *See* Restriction fragment length polymorphism
Population
effective population size, Metropolis-Hastings sampling, 1421
lethal-gene allelism in *Drosophila subobscura* colonizing America, 1297
linkage and limits to natural selection, 821
microsatellite variation in *Apis mellifera* populations, 679
mtDNA haplotype diversity in Ngŏbé Amerinds of Panama, 275
nucleotide variation at *vermilion* locus in geographi-

cally diverse *Drosophila melanogaster* and *D. simulans* populations, 1019
population structure in *Clarkia dudleyana*, comparison of population differentiation (F_{ST}) between allozymes and morphological traits, 733
recurrence equation for inbreeding coefficient for partially sib-mated population, 357
separating population structure from population history, cladistic analysis of geographic distribution of mtDNA haplotypes in *Amblystoma tigrinum*, 767
spatial distributions of genotypes under isolation by distance, 1431
spatial structure of two-locus genotypes under isolation by distance, 365
testing heterozygote excess and deficiency, 1413
Position effect variegation (PEV)
conservation of *trans*-inactivation of *brown* gene in *Drosophila*, 193
heterochromatic and euchromatic gene activity in *Drosophila melanogaster*, 1033
Protein(s)
agouti protein activity assay, 267
ribosomal protein RPS28 and translational accuracy in *Saccharomyces cerevisiae*, 1247
Protein glycosylation, vanadate-resistant mutants of *Saccharomyces cerevisiae*, 933

Quantitative trait loci (QTL)
analysis, dominance complementation as genetic basis of heterosis in rice, 745
interval mapping of QTL employing correlated trait complexes, 1137
mapping QTL on multiple traits, 1111

Random amplified polymorphic DNA (RAPD), approximate variance of nucleotide divergence between two sequences estimated from restriction fragment data (*letter*), 1443
RecBCD, in recombinagenic mismatch repair of UV-irradiated DNA, 1175
RecF, in recombinagenic mismatch repair of UV-irradiated DNA, 1175
Recombination
DNA gyrase-mediated oxolinic acid-induced illegitimate recombination in *Escherichia coli*, 889
frequency of homologous recombination, dependence on homology length, 797
homologous recombination and DNA integration and rearrangements in *Ashbya gossypii*, 973
IS*10*-stimulated recombination, 861
marker-dependent recombination in T4 bacteriophage, T4 DNA polymerase in, 13
meiosis-induced double-strand DNA breaks in *Saccharomyces cerevisiae*, 55
M26 recombination hot spot in *Schizosaccharomyces pombe*, 469
recJ suppression by alterations in DNA helicases, 27
recombinagenic mismatch repair of UV-irradiated DNA, 1175
recombination of Ty elements in yeast, double-strand break and, 67
between repeated sequences in yeast, role of DNA repair genes, 1199
Restriction fragment length polymorphism, telomere mapping in *Magnaporthe grisea*, 479
Retrotransposons, recombination of Ty elements induced by double-strand break, 67
RNA
ribosomal, multigene loci in wheat, 1367
5S RNA genes, intraspecific and intraspecific variation, 325
RNA polymerase II
Drosophila, carboxy-terminal repeat domain (CTD) function, 599
yeast, carboxy-terminal repeat domain (CTD) mutations, 1223

Saccharomyces cerevisiae
complexity of interaction between *RAD52* and *SRS2* (*letter*), 1441
DNA double-strand break repair, DNA synthesis errors in, 965
fimbrin-actin binding interaction in, genetic analysis, 91
genes required for $\alpha 2$ repression, 79
glycine catabolism, 1213
KRB1, second copy of *RPL4B* on fragment of chromosome *XII*, 129
meiosis, B-type cyclins for, 957
meiosis-induced double-strand DNA breaks in, 55
mitosis, B-type cyclins for, 957
mutational analysis for morphologic differentiation, 1259
pseudohyphal differentiation and *ELM* genes, 1259
rad52-20 suppression by *RAD1* and *MAT*, 115
recombination of Ty elements in, double-strand break and, 67
REV dependency of *rad* mutators in, 443
SCH9 kinase, 457
SIN4 regulation of *HIS4* expression, 103
SIN4-RGR1 complex in chromatin organization and transcriptional regulation, 47
suppression of *yme1* rho^0 slow growth in, 435
translational accuracy and ribosomal protein RPS28, 1247
vanadate-resistant mutants, protein glycosylation, sporulation and detergent resistance, 933
Schizosaccharomyces pombe
meiosis, *cdc2* and other genes in, 1235
M26 recombination hot spot, 469
sck1 (suppressor of loss of cAMP-dependent protein kinase activity) gene, 457
50S complex, morphogenesis, bacteriophage ϕX174 mutations affecting, 1167

Screening studies, modifiers of *Deformed (Def)* function in *Drosophila*, 1339
Selection
natural, limits, 821
polygenes and selection for gene conversion frequencies in *Ascobolus immersus*, 1277
positive selection for cold-sensitive myosin heavy chain mutants in Dictyostelium, 505
for translational efficiency, synonymous substitution rates in enterobacteria, 1407
Self-incompatibility system, *Brassica*, *S*-related genes, 1099
Serine biosynthesis, *Saccharomyces cerevisiae*, 1213
Sexual isolation, sequence divergence in *Bacillus* transformation and, 917
Sheep, autosomal genetic linkage map of sheep genome, 703
Signal transduction, *Suppressor of fused [su(fu)]* gene, 587
Solanum spp., relationship between mating system and Lyt element abundance in (*letter*), 418
Spatial autocorrelation analysis, patterns of DNA diversity, 811
Sporulation
in *Podospora anserina*, *mat* genes in, 493
vanadate-resistant mutants of *Saccharomyces cerevisiae*, 933
Stepwise mutation model, microsatellite variation in *Apis mellifera* populations, 679
Sterility, *Odysseus* locus of hybrid-male sterility in *Drosophila*, 201
Stress, expression of additive genetic variation under stress in *Drosophila melanogaster*, 1149
Superoxide dismutase, *ccSod1* and *ccSod2* genes in *Ceratitis capitata*, 697
Synaptic transmission, in *Caenorhabditis elegans*, 527

Telomere(s), mapping, in *Magnaporthe grisea*, 479
Temperature
latitudinal cline in body size of *Drosophila melanogaster*, 659
programmed heritable change in *r*-gene expression using temperature and light at specific developmental stages in maize seedlings, 1379
Tetrahymena thermophila, conjugation in, effect of nullisomic chromosome deficiencies, 989
Transcription
carboxy-terminal domain (CTD) of RNA polymerase II in, 1223
paramutation. *See* Paramutation
regulation, yeast *SIN4-RGR1* complex in, 47
regulation of *HIS4* expression by *Saccharomyces cerevisiae SIN4*, 103
α2 repression in *Saccharomyces cerevisiae*, 79
Rho-dependent transcription terminators in *nin* region of bacteriophage lambda, 875
short-patch reverse transcription in *E. coli*, 909
Transduction, Erf recombinase in bacteriophage P22-mediated plasmid transduction, 427
Transformation
genotypic, maternal, and grand maternal effects of immobilized derivatives of transposable element *mariner*, 183
sexual isolation and sequence divergence in *Bacillus* transformation, 917
Translation
ribosomal protein RPS28 and translational accuracy in *Saccharomyces cerevisiae*, 1247
selection for translational efficiency, synonymous substitution rates in enterobacteria, 1407
Transposable element
insertional effects on *Adh* gene expression in *Drosophila melanogaster*, 667
mariner, genotypic, maternal, and grand maternal effects of immobilized derivatives of, 183
MuDR, homologous transcripts encoded by, 1087
Mu1 insertional specificity in low copy number DNA, 315
transposable elements in inbreeding and outbreeding populations (*letter*), 415
Transposition, intermoleclar transposition of IS*10* and homologous recombination, 861
Tree, Scots pine, heterozygosity and fitness, 755
Tryptophan synthase beta subunit, mutants, in *Arabidopsis thaliana*, 303

Visual system, phylogenetic analysis of mitochondrial genomes from Leber hereditary optic neuropathy, 285

Weaver, Warren, quarreling geneticists and a diplomat (*Perspectives*), 421
Wheat
chromatid and chromosome type breakage-fusion-bridge cycles, 1069
intraspecific and intraspecific variation in 5S RNA genes, 325
ribosomal RNA multigene loci in wheat, 1367
Wolbachia infection
cytoplasmic incompatibility in *Drosophila sechellia* and *D. mauritiana*, 1307
cytoplasmic incompatibility in *Drosophila simulans*, 1319

X chromosome, effect on hybrid inviability/sterility, 389

Yeast. *See also Saccharomyces cerevisiae*
genetic control of recombinational between repeated sequences, 1199
RNA polymerase II CTD deletion and substitution mutations, construction and analysis, 1223
RTM1 (resistance to toxic molasses) gene, 945
Schizosaccharomyces pombe. *See Schizosaccharomyces pombe*